

In the specification:

Please amend the paragraph bridging pages 46-47 as follows:

The list of informative genes used in the AML vs. ALL predictor was highly instructive (FIG. 3B). In FIG. 3B, each row corresponds to a gene, with the columns corresponding to expression levels in different samples. Expression levels for each gene are normalized across the samples such that the mean is 0 and the standard deviation is 1. Expression levels greater than the mean are shaded in red, and those below the mean are shaded in blue. The scale indicates standard deviations above or below the mean. The top panel shows genes highly expressed in ALL; the bottom panel shows genes more highly expressed in AML. Note that while these genes as a group appear correlated with class, no single gene is uniformly expressed across the class, illustrating the value of a multi-gene prediction method. For a complete list of gene names, accession numbers and raw expression values, see <http://www.genome.wi.mit.edu/MPR>.